



E-ISSN: 2278-4136

P-ISSN: 2349-8234

www.phytojournal.com

JPP 2020; 9(3): 1384-1388

Received: 01-03-2020

Accepted: 03-04-2020

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AMMI Bi plot analysis for genotype x environment interaction on yield in rice (*Oryza sativa* L.) genotypes

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Abstract

There are several methods to estimate the stability of a genotype across environments or seasons by determining G x E interaction effects. Among these, AMMI analysis is the most recent and widely exploited in different crops for the identification of stable genotypes over locations as well as seasons. The main objective of the present study was to identify more high yielding stable promising genotypes and to determine the best seasons would be adapted by AMMI model. In the present investigation, the experiment material comprised a total of seven rice genotypes evaluated using randomized complete block design with three replications during three seasons *rabi* 2014-15, *kharif* 2015 and *rabi* 2015-16. Pooled analysis of variance indicated that significance variance among genotypes, seasons and genotype x environment interactions indicated the usefulness of AMMI model. Yield stability and adaptability of yield performance were analyzed by additive main effects and multiplicative interaction (AMMI) model. Among the rice genotypes, G1 (WGL-1097), G5 (WGL-1101) and G4 (WGL-1100) exhibited high yield, out of which G1 being the overall best genotype in terms of yield. As per AMMI 2 biplot, G7 (WGL-1010), G6 (WGL-1102), G1 (WGL-1097) and G4 (WGL-1100) had more responsive since they were away from the origin whereas the genotypes G3 (WGL-1099) and G2 (WGL-1098) were close to the origin and hence they were less sensitive to environmental interactive forces. What-won-where biplot indicated that three environments fall into two mega environments. Hence the genotype G1 (WGL-1097) was the winner in the environments E1 and E3 where as the genotype G2 (WGL-1098) was the winner in the environment E2. This pattern suggests that the target environment may consist of two mega environments and that different genotypes should be selected for each environment.

Keywords: Rice, genotype x environment interaction, AMMI biplots, what-won-where biplot

Introduction

Yield in rice depends on genotype, environment and management practices and their interaction with each other (Messina *et al.*, 2009) ^[11]. Information of genotype x environment interaction leads to successful evaluation of stable genotypes, which could be used for general cultivation (Anowara Akter *et al.*, 2015) ^[4]. The interplay in the effect of genetic and non-genetic on development is termed as G x E interaction. G x E interactions are of major consequences to the breeder in the process of evolution of improved varieties. So, phenotypes are the mixture of Genotype (G), Environment (E) components and interactions (G x E) between them (Darai *et al.*, 2017) ^[6]. There are several methods to estimate the stability of a genotype across environments by determining G x E interaction effects. Among these, AMMI analysis is the most recent and widely exploited in different crops for the identification of stable genotypes over locations. The results of AMMI (Additive Main Effects and Multiplicative Interaction) analysis are useful in identifying the stable genotypes to specific environments which can be utilized in breeding program.

AMMI is especially effective tool where the assumption of linearity of the response of genotype to a change in the environment is not fulfilled (Zobel *et al.*, 1988, Yan and Hunt, 1998) ^[16, 15] and which usually separates the interaction part of the multiplicative components into the additive main effects by principal component analysis. The AMMI model is a hybrid model involving both additive and multiplicative components of two way data structure which enabled a breeder to get precise prediction on genotypic potentiality and environmental influences on it. AMMI uses ordinary ANOVA to analyze the main effects (additive part) and principal component analysis (PCA) to analyze the non additive residual left over by the ANOVA (Gauch, 1993) ^[8].

The main objective of the present study was to identify more high yielding stable promising genotypes and to determine the seasons would be adapted by AMMI model. (Anowara Akter *et al.*, 2014) ^[3].

Therefore, using the AMMI analysis with biplot facility, yield data were analyzed to determine the nature and magnitude of G x E interaction effects on grain yield in diverse seasons.

Materials and Methods

In the present investigation, the experiment material comprised a total of seven rice genotypes which were evaluated through observational, preliminary and advanced yield trials for yield, yield attributing traits. The present investigation was carried out at the Regional Agricultural Research Station, Warangal, which is located at an altitude of 304 M above MSL, 17.97° N latitude and 79.60° E longitude during three seasons *rabi*, 2014-15, *khariif*, 2015 and *rabi*, 2015-16. The main crop seasons in Telangana State can be called as *khariif* (June-Dec) and *rabi* (Nov-April) seasons. The experiments were laid in randomized block design with three replications. Standard package of practices were followed to maintain a good crop in the field. The data was subjected to analysis of variance and then taken for AMMI analysis for identification of stable genotypes.

Statistical analysis

The pooled analysis of variance was proceeded to look at G x E and stability of the genotypes across all environments. Analysis of variance was significant for genotypes, environments and (G x E) components indicating the use fullness of AMMI analysis in identifying the stable genotypes. The AMMI model, which combines standard analysis of variance with PC analysis (Zobel *et al.*, 1988) [16], was used to investigate of G x E interaction. In AMMI model the contribution of each genotype and each environment to the GEI is assessed by use of the biplot graph display in which yield means are plotted against the scores of the IPCA1 (Zobel *et al.*, 1988) [16]. ANOVA and Stability analysis for yield trait was carried out by using the AMMI model R-packages 1.5, PB Tools 1.4 version IRRI. The G x E interaction was analyzed following AMMI biplot (Gauch, 1989) [9].

Results and Discussions

The details of genotypes and environments are presented in table 1. The pooled analysis of variance for yield over three environments is presented in table 2. Analysis of variance was significant for genotypes, environments and (G x E) components indicating the use fullness of AMMI analysis in identifying the stable genotypes. The additive main effects and multiplicative interaction (AMMI) model calculates genotypes and environment additive (main) effects using

analysis of variance and then analyze the residual from this model using principal component analysis (PCA). The AMMI model is a graphical representation of the numerical results (biplot analysis), allows a straight forward interpretation of the underlying causes of G x E interaction. Genotypes yield mean data along with IPCA 1 and IPCA 2 values for seven genotypes are presented in Table 3. AMMI procedure has been clearly demonstrated by various authors in selection of stable rice genotypes (Yan and Hunt, 2001, Das *et al.*, 2009, Islam *et al.*, 2014 and Bharat Taindu Jain *et al.*, 2018) [15, 7, 10, 5].

Table 1: The codes and names of rice genotypes and environments

Genotypes Codes	Genotypes Names	Environment Codes	Environment Names
G1	WGL-1097	E1	<i>Rabi</i> , 2014-15
G2	WGL-1098	E2	<i>Khariif</i> , 2015
G3	WGL-1099	E3	<i>Rabi</i> , 2015-16
G4	WGL-1100		
G5	WGL-1101		
G6	WGL-1102		
G7	MTU-1010		

Table 2: AMMI Analysis of Variance for yield (kg/ha) of seven genotypes over three environments

Source	D.F	S.S	M.S
Varieties	6	17608976.41	2934829.40**
Environments	2	99510320.66	49755160.33**
Varieties X Environments	12	26265005.77	2188750.48**
IPCA1	7	19085626.00	2726518.00
IPCA2	5	7179380.00	1435876.00
Error	42	7504970.00	178689.76
Total	62	150889272.85	-

The analysis showed that variations due to G, E and G x E were significant ($P < 0.01$).

Table 3: Mean grain yield (Kg/ha), IPCA1 and IPCA2 values of the seven rice genotypes

S. No	Genotype	Mean	IPCA1	IPCA2
1	WGL-1097	7605	-10.70	17.06
2	WGL-1098	6688	32.25	2.48
3	WGL-1099	6294	26.42	2.31
4	WGL-1100	7011	-13.99	-15.58
5	WGL-1101	7138	-15.72	-4.64
6	WGL-1102	6115	-2.31	-19.89
7	MTU-1010	6115	-11.30	26.85

AMMI 1 Biplot

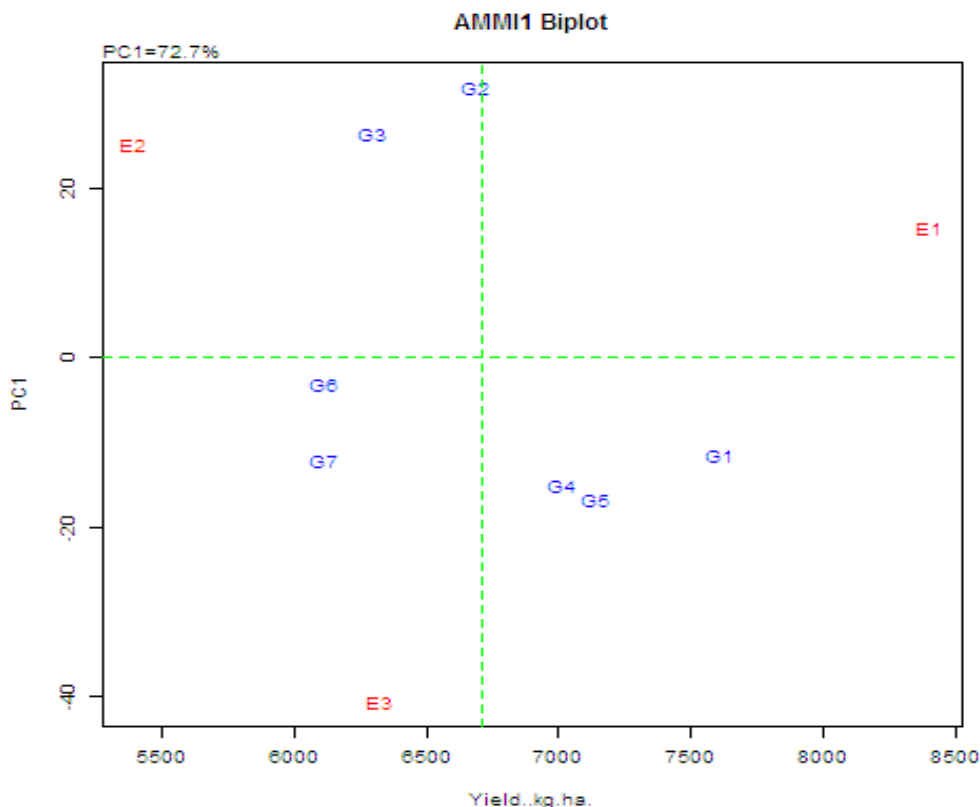


Fig 1: Biplot of the first interaction principal component axis (IPCA1) versus mean yields.

In AMMI-I biplot (Figure1), Genotypes and environments on the same parallel lines have similar yields and a genotype or environment on the right side of the midpoint of this axis has higher yields than those of left hand side. Accordingly, among the rice genotypes, G1 (WGL-1097), G5 (WGL-1101) and G4 (WGL-1100) exhibited high yield of positive IPCA1 score, out of which G1 had high IPCA1 scores being the overall best genotype. The rice genotypes G3 (WGL-1099), G6 (WGL-

1102) and G7 (MTU-1010) recorded the yield below the mean yield. Of the environments, however, E2 is most favorable environment for genotype G2 and E3 (*rabi*, 2015-16) for genotypes G6 (WGL-1102) and G7 (MTU-1010). Adugna, 2007^[1] and Anandan *et al.*, 2009^[2] reported similar pattern of interactions.

AMMI 2 Biplot

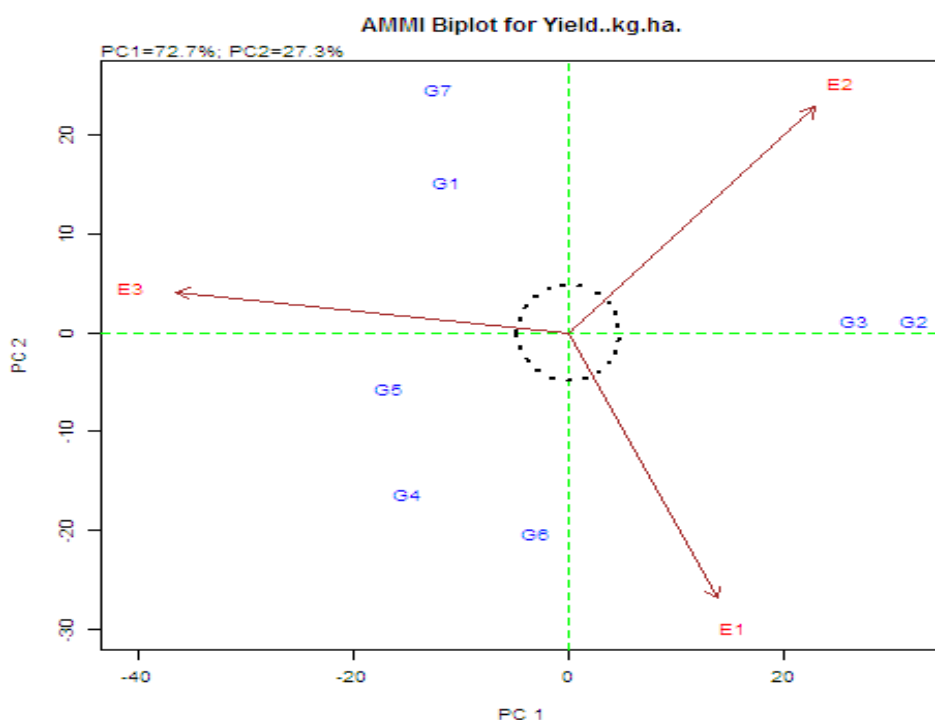


Fig 2: Biplot of the first interaction principal component axis (IPCA1) versus the second interaction principal component axis (IPCA2) for rice genotypes.

In AMMI 2 biplot (Figure2), the environmental scores are joined to the origin by side lines. Sites with short spokes do not exert strong interactive forces. Those with long spokes exert strong interaction (Tadesse Lakew *et al.*, 2017^[12]). All the environments E1, E2 and E3 exerted strong interaction forces. On the other hand, the genotypes near the origin are not sensitive to environmental interaction and those distant from the origins are sensitive and have large interaction.

Accordingly, G7 (WGL-1010), G6 (WGL-1102), G1 (WGL-1097) and G4 (WGL-1100) had more responsive since they were away from the origin whereas the genotypes G3 (WGL-1099) and G2 (WGL-1098) were close to the origin and hence they were less sensitive to environmental interactive forces.

What-won-where Biplot

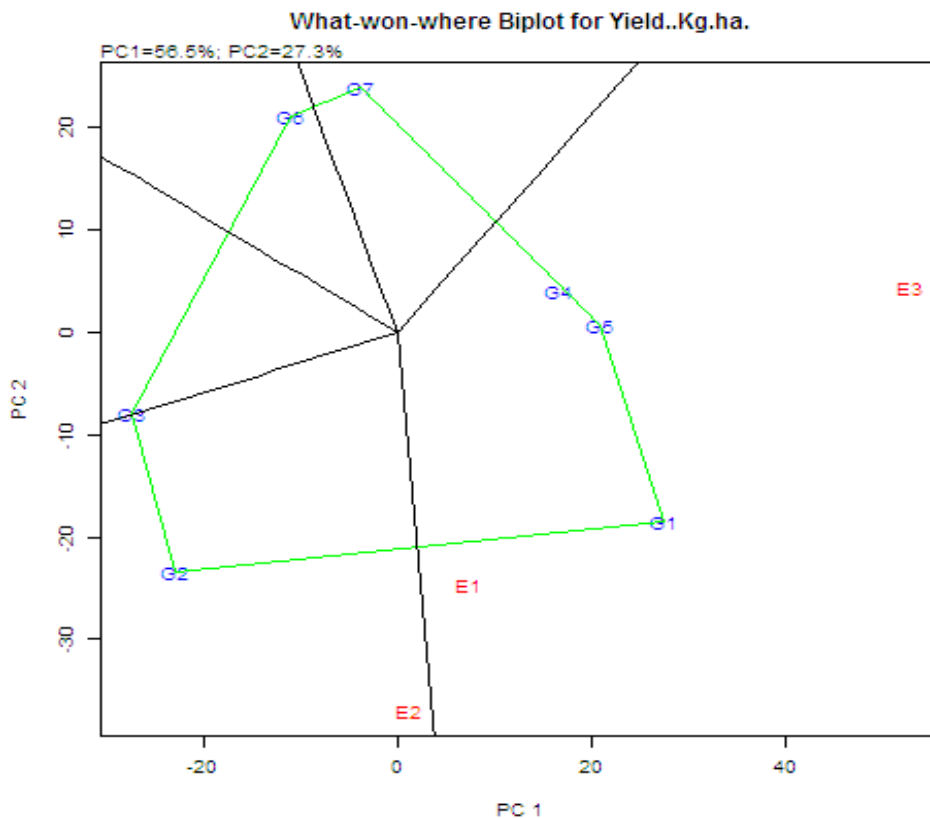


Fig 3: The What-won-where view of the GGE biplot to show which genotype performed best in which environments.

What –won-where GGE biplot has the ability to show the what - won – where pattern of a genotype by environment data set. A polygon is first drawn on genotypes that are furthest from the biplot origin so that all other genotypes are contained within the polygon. The perpendicular lines to each side of the polygon are drawn, starting from the biplot origin. (Weikal Yan and Tinker, 2006^[13]). Genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments. Accordingly, the rice genotypes G1 (WGL-1097) was better in the environments E1 and E3, whereas the genotype G2 (WGL-1098) was better in the environment E2 (Fig no. 3). The rice genotype G5 (WGL-1101) and G4 (WGL-1100) also perform better in environments E1 and E3 next to G1. Three environments fall into two mega environments. Hence the genotype G1 (WGL-1097) was the winner in the environments E1 and E3 whereas the genotype G2 (WGL-1098) was the winner in the environment E2. This pattern suggests that the target environment may consist of two mega environments and that different genotypes should be selected for each environment. Accordingly, *rabi* season is better to perform well for the genotypes G1 (WGL-1097).

Acknowledgment

The authors are highly thankful to ICAR-IIRR, Hyderabad for providing material and financial support.

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